

MORPHOLOGICAL CHARACTERIZATION AND GENETIC DIVERSITY ASSESSMENT OF APULIAN ALMOND GERMPLASM

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Prunus dulcis, microsatellites, phenotypic descriptors, local biodiversity safeguard

Almond (*Prunus amygdalus* Batsch, syn. *Prunus dulcis* Miller D.A.Webb, syn. *Amygdalus communis* L.) is probably the oldest tree nut crop to be domesticated, as the first signs of its cultivation appeared around 3000 B.C. Native to Central Asia, it spreads over several centuries to the West, mainly toward the Mediterranean basin and in particular to Southern Italy, where it is largely cultivated for its edible fruits and kernels. As good source of high-quality oil and natural antioxidants with bioactive properties, almond has been always widely used in food as well as in pharmaceutical and cosmetic industries.

In last decades, a drastic decline in Italian almond production occurred due to low and variable yields, inefficient orchard management, emergence of new diseases and unfavourable import/export conditions. These problems have caused the abandonment of many local cultivars and increased the risk of genetic erosion. To reverse this process and to prevent the extinction of native almond trees over the years, a classification of local cultivars and the creation of almond germplasm collections with a wide genetic diversity have been started in Italy. In particular, given the economic and cultural importance of almond cultivation in Apulia region, this work aimed to study the genetic structure of Apulian almond germplasm and to safeguard ancient and local genotypes, also for breeding purposes.

Almond biodiversity was estimated by both morphological and molecular analysis. A set of 18 SSR, chosen on their dispersal map location, was used to assess the genetic variability of 100 genotypes and unique profiles were obtained for each. The LRM (Lynch & Ritland Method) values allowed highlighting several cases of synonymy and homonymy; moreover, the Neighbor Joining and STRUCTURE analysis have revealed the genetic distance among individuals and different levels of clusterization. Finally, the association between the genetic variability of the analysed collection with significant differences in some morphological traits was investigated by means of 34 phenotypic descriptors relating to branch, flower, leaf, and fruit morphology.